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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Golstein, Pierre
Rouvier, Eric
Fossiez, Francois
Lebecque, Serge J.E.
Djossou, Odile
Banchereau, Jacques

(ii) TITLE OF INVENTION: Purified Mammalian CTLA-8 Antigens and
Related Reagents

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Townsend and Townsend and Crew LLP
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(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09929612
(B) FILING DATE: 13-AUG-2001
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/077,203
(B) FILING DATE: 14-JUN-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/177,747
(B) FILING DATE: 05-JAN-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/250,846
(B) FILING DATE: 27-MAY-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/432,994
(B) FILING DATE: 02-MAY-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/432,994
(B) FILING DATE: 22-JUN-1998

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Weber, Kenneth A.
(B) REGISTRATION NUMBER: 31,677
(C) REFERENCE/DOCKET NUMBER: 015631-003115US

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 576-0200
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 12..464
(D) OTHER INFORMATION: /product= "mouse/rat CTLA-8"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCATC C ATG TGC CTG ATG CTG TTG CTG CTA CTG AAC CTG GAG GCT	50
Met Cys Leu Met Leu Leu Leu Leu Leu Asn Leu Glu Ala	
1 5 10	
ACA GTG AAG GCA GCG GTA CTC ATC CCT CAA AGT TCA GTG TGT CCA AAC	98
Thr Val Lys Ala Ala Val Leu Ile Pro Gln Ser Ser Val Cys Pro Asn	
15 20 25	
GCC GAG GCC AAT AAC TTT CTC CAG AAC GTG AAG GTC AAC CTG AAA GTC	146
Ala Glu Ala Asn Asn Phe Leu Gln Asn Val Lys Val Asn Leu Lys Val	
30 35 40 45	
ATC AAC TCC CTT AGC TCA AAA GCG AGC TCC AGA AGG CCC TCA GAC TAC	194
Ile Asn Ser Leu Ser Ser Lys Ala Ser Ser Arg Arg Pro Ser Asp Tyr	
50 55 60	
CTC AAC CGT TCC ACT TCA CCC TGG ACT CTG AGC CGC AAT GAG GAC CCT	242
Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu Ser Arg Asn Glu Asp Pro	
65 70 75	
GAT AGA TAT CCT TCT GTG ATC TGG GAG GCA CAG TGC CGC CAC CAG CGC	290
Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln Cys Arg His Gln Arg	
80 85 90	
TGT GTC AAC GCT GAG GGG AAG TTG GAC CAC CAC ATG AAT TCT GTT CTC	338
Cys Val Asn Ala Glu Gly Lys Leu Asp His His Met Asn Ser Val Leu	
95 100 105	

ATC	CAG	CAA	GAG	ATC	CTG	GTC	CTG	AAG	AGG	GAG	CCT	GAG	AAG	TGC	CCC		386		
Ile	Gln	Gln	Glu	Ile	Leu	Val	Leu	Lys	Arg	Glu	Pro	Glu	Lys	Cys	Pro				
110					115					120					125				
TTC	ACT	TTC	CGG	GTG	GAG	AAG	ATG	CTG	GTG	GGC	GTG	GGC	TGC	ACC	TGC		434		
Phe	Thr	Phe	Arg	Val	Glu	Lys	Met	Leu	Val	Gly	Val	Gly	Cys	Thr	Cys				
				130						135					140				
GTT	TCC	TCT	ATT	GTC	CGC	CAT	GCG	TCC	TAAACAGAGA				CCTGAGGCTA					481	
Val	Ser	Ser	Ile	Val	Arg	His	Ala	Ser											
			145					150											
GCCCCTAAGA			AACCCCTGCG			TTTCTCTGCA			AACTTCCTTG			TCTTTTTAAA			ACAG TTCACA			541	
GTTGAATCTC			AGCAAGTGAT			ATGGATT TAA			AGGCGGGGTT			AGAATTGTCT			GCCTTCCACC			601	
CTGAAAAGAA			GGCGCAGAGG			GGATATAAAAT			TGCTTCTTGT			TTTTCTGTGG			GCTTTAAATT			661	
ATTTATGTAT			T TACTCTATC			CCGAGATAAC			TTTGAGGCAT			AAGTTATTTT			AATGAATTAT			721	
CTACATTATT			ATTATGTTTC			TTAATGCAGA			AGACAAAATT			CAAGACTAAG			AAATTTTATT			781	
ATTTAAAAGG			TAAAACCTAT			ATTTATATGA			GCTATTTTATG			GGTCTATTTA			TTTTTCTTCA			841	
GTGCTAAGAT			CATGATTATC			AGATCTACCT			AAGGAAGTCC			TAAATAATAT			TAAATATTAA			901	
TTGAAATTTT			AGTTTTACTA			TTTGCTTATT			TAAGGTTCCT			TCCTCTGAAT			GGTGTGAAAT			961	
CAAACCTCGT			TTTATGTTTT			TAAATTATTG			AGGCTTCGAA			AAATTGGGCA			ATTTAGCTTC			1021	
CTACTGTGTG			TTTAAAAACC			TTGTAAACAAT			ATCACTATAA			TAAATTTTTG			GAAGAAAAAT			1080	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Cys Leu Met Leu Leu Leu Leu Leu Asn Leu Glu Ala Thr Val Lys
1 5 10 15

Ala Ala Val Leu Ile Pro Gln Ser Ser Val Cys Pro Asn Ala Glu Ala
20 25 30

Asn Asn Phe Leu Gln Asn Val Lys Val Asn Leu Lys Val Ile Asn Ser
35 40 45

Leu Ser Ser Lys Ala Ser Ser Arg Arg Pro Ser Asp Tyr Leu Asn Arg
50 55 60

Ser Thr Ser Pro Trp Thr Leu Ser Arg Asn Glu Asp Pro Asp Arg Tyr
 65 70 75 80
 Pro Ser Val Ile Trp Glu Ala Gln Cys Arg His Gln Arg Cys Val Asn
 85 90 95
 Ala Glu Gly Lys Leu Asp His His Met Asn Ser Val Leu Ile Gln Gln
 100 105 110
 Glu Ile Leu Val Leu Lys Arg Glu Pro Glu Lys Cys Pro Phe Thr Phe
 115 120 125
 Arg Val Glu Lys Met Leu Val Gly Val Gly Cys Thr Cys Val Ser Ser
 130 135 140
 Ile Val Arg His Ala Ser
 145 150

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1574..2029
- (D) OTHER INFORMATION: /product= "Saimiriine herpesvirus 2
immediate-early protein"
/note= "open reading frame 2 (ORF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCTTCATGC AAATACATCT TATCTTACCA GATTCTCGCC TCATTGCAA ACATGCCTCA	60
TCTTTTGAGA AGAAACGCAA TTCGAACTTC TTCTAATGCT CCTGAAGAGC AGCCTGTGCT	120
GCAGCCTGAG CTTGATGCTA TTGAAGAGCT AGAATAAGAG CTATTTTTTG ACGATGGGTG	180
CTGCCTTTCT GTTCAAGAAA TCTGCTTAAT TGTCTTGGA TTCTTATTGT TTCTGCTAGC	240
TGTAATTGTT TTTTATAACT ATACAGACAC AGATCAATTT GTGAAGCTGA CACATCTTAT	300
GAGCCACAAA AATTCTATCA AAGGACCTTT TGATCTTTAA GGTATGTACT CATAATTTTA	360
TTTTTTTATT TCTAAAACAA TCTTAGTATA TATAATTAAT ACAAATTTTA GAAAATACTA	420
TAATAAATAT TGAAAGCTGT ATTTACATTG TAACTATAT ATAGGCAATG TAAAGTCATT	480
CTAACTTTAG GTTTGCTTTA CCTGTTACAG AACTTCACC TGTGTGTCAA GAGCTGCAAA	540

CATGGCTTTA GACTTAAGAA ATCTTAAACA CCTGACTGCT AACTTCAGTT TTAGAATAAT	600
GATATGGATT ATGCTATGTT TGGCTCTACC TACTGATAGT AAACCTATTT CAACAACTGA	660
AGCTCCAATA CTAAACATAA CACAATCTCC AAGTTTGAAC ATCTCATCAC CTTCTACTTT	720
AGAACCTTCA GAGCCTCTTA AAAACTGTAC AACATTCTTA GACTTACTTT GGCAGCGGCT	780
GGGCGAGAAC GCTTCTATAA AGGACTTGAT GTTAACATTA CAACGAGAAG AAGTCCACGG	840
AAGAATGACT ACACTTCCTT CACCTAGACC AAGCAGTAAA GTTGAAGAAC AACAGTTACA	900
AAGACCTAGA AACTTACTGC CTACTGCTGT CGGGCCACCT CATGTCAAAT ATAGACTATA	960
TAATCGCTTA TGGGAAGCTC CTAAAGGAGC TGATGTTAAT GGTA AACCTA TACAATTTGA	1020
TGACCCTCCT CTTCCTTATA CAGGGGCATA TAATGATGAT GGTGTTTTAA TGGTTAATAT	1080
TAATGGAAAA CATGTGAGGT TTGATAGCTT GTCTTATTGG GAAAGAATTA AAAGATCTGG	1140
TACCCCATGG TGTATAAAGA CACCAAGTGA AAAAGCAGCA ATATTGAAGC AGCTTTTAAA	1200
AGCTGAAAAA AAATGTAGGA CTACTTCTAA ACGTATCACT GAGTTAGAAG AGCAGATTAA	1260
AGAACTAGAA AAAACTAGTA CATCTCCATA GATTACTGTT AGAATGTGTT TATCATACTA	1320
AAATAAATGC TTTATGTATT GCAATATTAC TTGTTTGCTA TGACTTTGGT ATATGAAATG	1380
CAAATCTTAA ATAAAAAGTT TTTGTCTAGT ATTGGCGTCA CTGTATTTTA CTAGCAAAAA	1440
TATATAAATT GTTATGTAGC AAGAAGTTTG TATCAATATA AAAACTCTAA AGTATATAAA	1500
CAAACATTCA ATTAGTGTA ATCATAGCAA GCATATCTTT TCATACGTGT CTAGTTAATT	1560
TAAAGAATTA ATT ATG ACA TTT AGA ATG ACT TCA CTT GTG TTA CTT CTG	1609
Met Thr Phe Arg Met Thr Ser Leu Val Leu Leu Leu	
1 5 10	
CTG CTG AGC ATA GAT TGT ATA GTA AAG TCA GAA ATA ACA AGC GCA CAA	1657
Leu Leu Ser Ile Asp Cys Ile Val Lys Ser Glu Ile Thr Ser Ala Gln	
15 20 25	
ACC CCA AGA TGC TTA GCT GCT AAC AAT AGC TTT CCA CGG TCT GTG ATG	1705
Thr Pro Arg Cys Leu Ala Ala Asn Asn Ser Phe Pro Arg Ser Val Met	
30 35 40	
GTT ACT TTG AGC ATC CGT AAC TGG AAT ACT AGT TCT AAA AGG GCT TCA	1753
Val Thr Leu Ser Ile Arg Asn Trp Asn Thr Ser Ser Lys Arg Ala Ser	
45 50 55 60	
GAC TAC TAC AAT AGA TCT ACG TCT CCT TGG ACT CTC CAT CGC AAT GAA	1801
Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu	
65 70 75	
GAT CAA GAT AGA TAT CCC TCT GTG ATT TGG GAA GCA AAG TGT CGC TAC	1849
Asp Gln Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg Tyr	

80	85	90	
TTA GGA TGT GTT AAT GCT GAT GGG AAT GTA GAC TAC CAC ATG AAC TCA			1897
Leu Gly Cys Val Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser			
95	100	105	
GTC CCT ATC CAA CAA GAG ATT CTA GTG GTG CGC AAA GGG CAT CAA CCC			1945
Val Pro Ile Gln Gln Glu Ile Leu Val Val Arg Lys Gly His Gln Pro			
110	115	120	
TGC CCT AAT TCA TTT AGG CTA GAG AAG ATG CTA GTG ACT GTA GGC TGC			1993
Cys Pro Asn Ser Phe Arg Leu Glu Lys Met Leu Val Thr Val Gly Cys			
125	130	135	140
ACA TGC GTT ACT CCC ATT GTT CAC AAT GTA GAC TAAAAGCTAT CTAAATTTTG			2046
Thr Cys Val Thr Pro Ile Val His Asn Val Asp			
145	150		
AAAATTAACA TTTCATAAA AAACAAAAAC TTGATTTTTT TCTTTTAAAT AAAAAAAGTT			2106
TAATATAAGT TCTGGCTTGT TTGGTTTTTG ACTAATCAAT GTAGATCACA CTTGTGATCT			2166
TAGCTCTCGG GAAGCAATGT AAGAAAATAT ATTAACTTA AGAGTTTTAG ACTTGCTTGA			2226
GTTTTATGAG TAAAAAACAA AGAATAAGCA CAGCTTCTTG TATCTTCTTT TAAAACTTT			2286
AAGTTATTTA TGTATTTAAT ATAATCTAAT GTTCTTAAA CATGTTGAGT TTGAGGTCCA			2346
CTAATACAAC ATTATAATTT TTTCTGTTAT AACACTTTTG CAAGAAGAAC TCATTTTATA			2406
GAAAATGAGC AGTATTCAAA AAAAATGTTT GATATGCTGT AATATTGGAG AGGAAGAACT			2466
TTTACAAGCA TGTGATTGTC CTAGCAGAGT CCATCATACA TGCTTACAAA GTCA			2520

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Phe Arg Met Thr Ser Leu Val Leu Leu Leu Leu Leu Ser Ile			
1	5	10	15
Asp Cys Ile Val Lys Ser Glu Ile Thr Ser Ala Gln Thr Pro Arg Cys			
20	25	30	
Leu Ala Ala Asn Asn Ser Phe Pro Arg Ser Val Met Val Thr Leu Ser			
35	40	45	
Ile Arg Asn Trp Asn Thr Ser Ser Lys Arg Ala Ser Asp Tyr Tyr Asn			
50	55	60	

Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu Asp Gln Asp Arg
65 70 75 80

Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg Tyr Leu Gly Cys Val
85 90 95

Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln
100 105 110

Gln Glu Ile Leu Val Val Arg Lys Gly His Gln Pro Cys Pro Asn Ser
115 120 125

Phe Arg Leu Glu Lys Met Leu Val Thr Val Gly Cys Thr Cys Val Thr
130 135 140

Pro Ile Val His Asn Val Asp
145 150

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..237
- (D) OTHER INFORMATION: /product= "human CTLA-8 fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

MGC AAT GAG GAC CCT GAG AGA TAT CCC TCT GTG ATC TGG GAG GCA AAG	48
Xaa Asn Glu Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys	
1 5 10 15	
TGC CGC CAC TTG GGC TGC ATC AAC GCT GAT GGG AAC GTG GAC TAC CAC	96
Cys Arg His Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His	
20 25 30	
ATG AAC TCT GTC CCC ATC CAG CAA GAG ATC CTG GTC CTG CGC AGG GAG	144
Met Asn Ser Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu	
35 40 45	
CCT CCA CAC TGC CCC AAC TCC TTC CGG CTG GAG AAG ATA CTG GTG TCC	192
Pro Pro His Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser	
50 55 60	
GTG GGC TGC ACC TGT GTC ACC CCG ATT GTC CAC CAT GTG GCC	234
Val Gly Cys Thr Cys Val Thr Pro Ile Val His His Val Ala	

TAA

237

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Arg"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Asn Glu Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys
1 5 10 15
Cys Arg His Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His
20 25 30
Met Asn Ser Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu
35 40 45
Pro Pro His Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser
50 55 60
Val Gly Cys Thr Cys Val Thr Pro Ile Val His His Val Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: /note= "full length human CTLA-8 clone"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 43..510

(D) OTHER INFORMATION: /product= "human CTLA-8"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCACAAACT CATCCATCCC CAGTTGATTG GAAGAAACAA CG ATG ACT CCT GGG	54
Met Thr Pro Gly	
1	
AAG ACC TCA TTG GTG TCA CTG CTA CTG CTG CTG AGC CTG GAG GCC ATA	102
Lys Thr Ser Leu Val Ser Leu Leu Leu Leu Leu Ser Leu Glu Ala Ile	
5 10 15 20	
GTG AAG GCA GGA ATC ACA ATC CCA CGA AAT CCA GGA TGC CCA AAT TCT	150
Val Lys Ala Gly Ile Thr Ile Pro Arg Asn Pro Gly Cys Pro Asn Ser	
25 30 35	
GAG GAC AAG AAC TTC CCC CGG ACT GTG ATG GTC AAC CTG AAC ATC CAT	198
Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn Leu Asn Ile His	
40 45 50	
AAC CGG AAT ACC AAT ACC AAT CCC AAA AGG TCC TCA GAT TAC TAC AAC	246
Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser Asp Tyr Tyr Asn	
55 60 65	
CGA TCC ACC TCA CCT TGG AAT CTC CAC CGC AAT GAG GAC CCT GAG AGA	294
Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu Asp Pro Glu Arg	
70 75 80	
TAT CCC TCT GTG ATC TGG GAG GCA AAG TGC CGC CAC TTG GGC TGC ATC	342
Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His Leu Gly Cys Ile	
85 90 95 100	
AAC GCT GAT GGG AAC GTG GAC TAC CAC ATG AAC TCT GTC CCC ATC CAG	390
Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln	
105 110 115	
CAA GAG ATC CTG GTC CTG CGC AGG GAG CCT CCA CAC TGC CCC AAC TCC	438
Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His Cys Pro Asn Ser	
120 125 130	
TTC CGG CTG GAG AAG ATA CTG GTG TCC GTG GGC TGC ACC TGT GTC ACC	486
Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys Thr Cys Val Thr	
135 140 145	
CCG ATT GTC CAC CAT GTG GCC TAA	510
Pro Ile Val His His Val Ala	
150 155	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: ami